

Figure 1

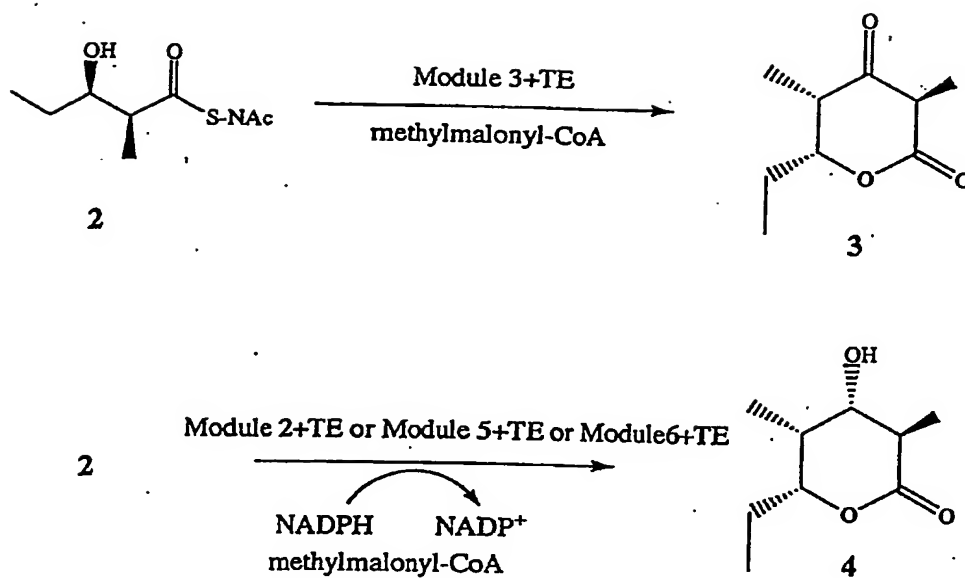


Figure 2

(a) INTRA-POLYPEPTIDE LINKER

M2ery: GGATGAEQAAPATT..APVD  
M4ery: VGDAĐ..QAA.VRVVGAA.DES  
M6ery: VGAAEAEQA.PALVREVPKDAD  
M2rif: FGSA.A.NR.PAEIGTAAAE  
M3rif: LG..ER.PAAPAPVTRDVSD  
M5rif: GETVAGAPATPVTTVADAG  
M3rap: .ELFTGENPAPVRGPVSAVGQD  
M4rap: .ELFTGENPAPVRGPVSVVGQD  
M7rap: .ELFTGENPAPVRGPVSA.GQD

(b) N-TERMINAL INTER-POLYPEPTIDE LINKER

M3ery: .....VTD SE KVAEYLRR .ATL DLRAAR QRIRE..LES  
M5ery: MSGDNGM.TE E.KLRRYLKR TVT.ELDSVT ARLRE..VEH RAG  
M4rif: .....MSAPNE QIVDAL.R ASLKE....N VRLQQENSAL AAAAA  
M7rif: .....VSASYE KVVEAL.R KSLEE....V GTLKKRNRQL ADAAG  
M8rif: .....V.AD EGQLRDYLKR .AIADARDAR TRLRE..VEE QAR  
M9rif: .....MATD E.KLLKYLR .VTAE LHS.. ..LRKQGARH .AD  
M5rap: .....MR.. EDQLLDAL.R KSVKE....N ARLRKANTSL RAAMD  
M11rap: .....M.PEQD KVVEYL.R WATAELHTTR AKL.....EA LAAANT

Figure 3



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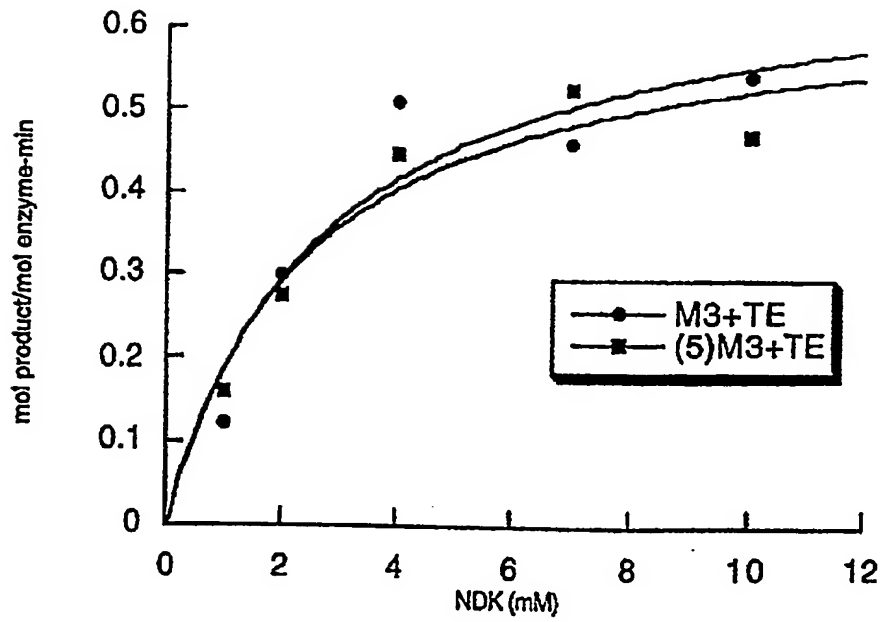
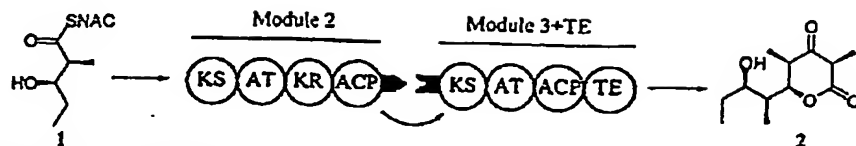
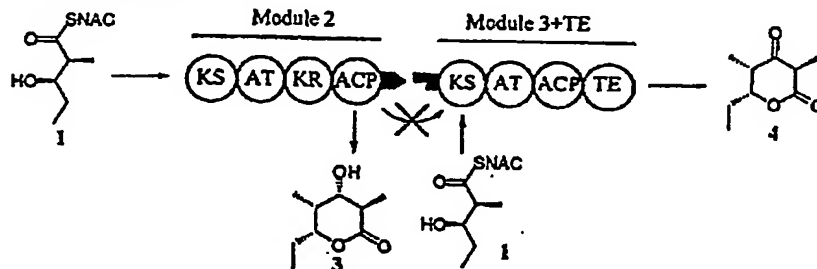


Figure 5

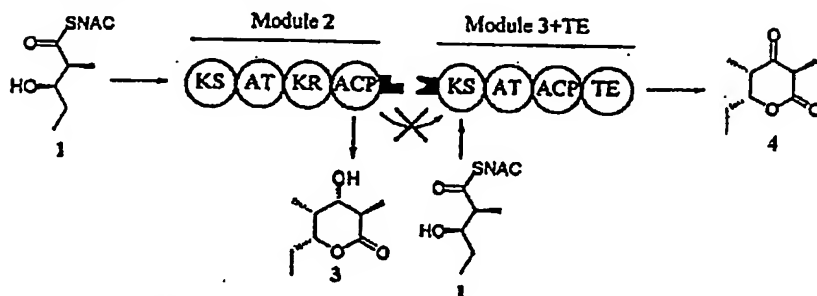
**A. M2 and M3+TE**



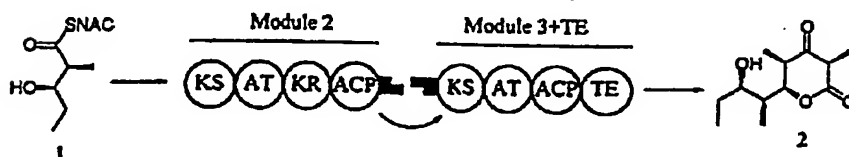
**B. M2 and (5)M3+TE**



**C. M2(4) and M3+TE**



**D. M2(4) and (5)M3+TE**



**Figure 6**

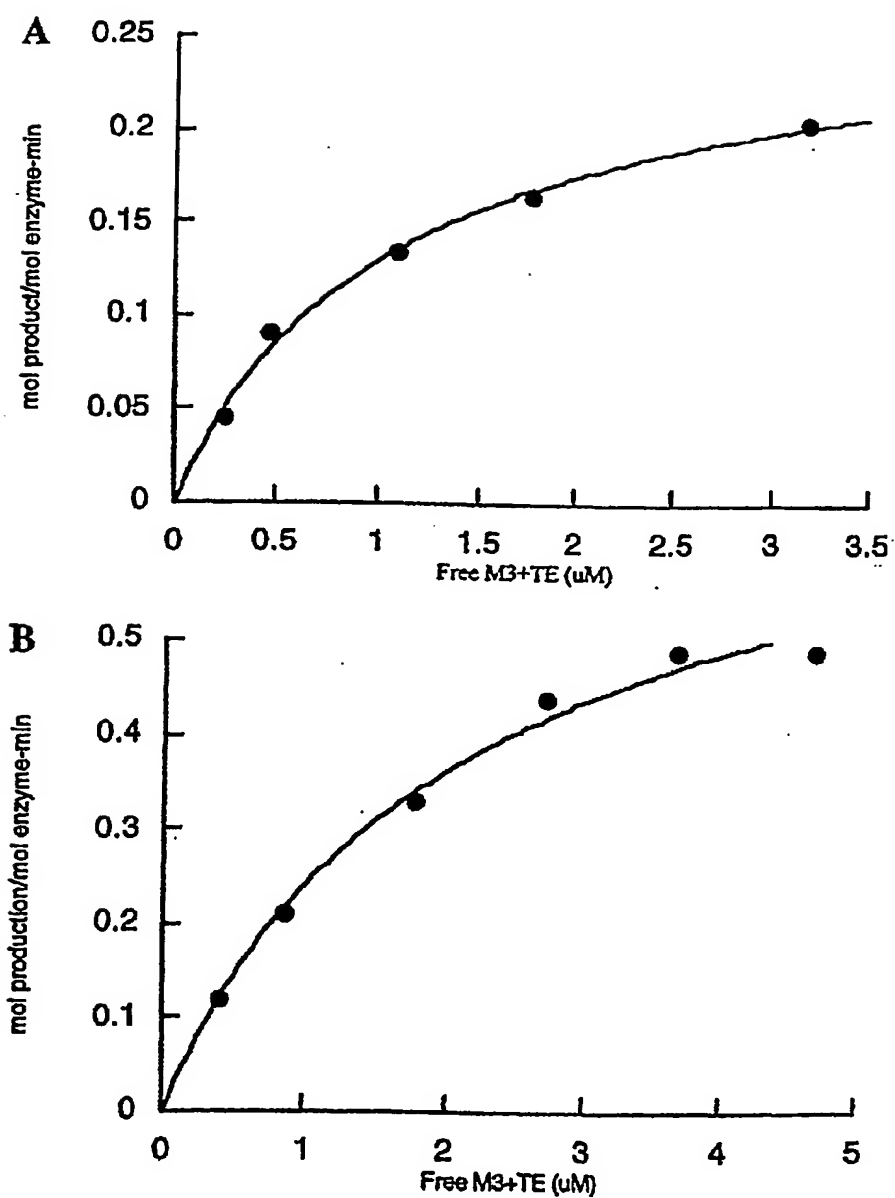


Figure 7

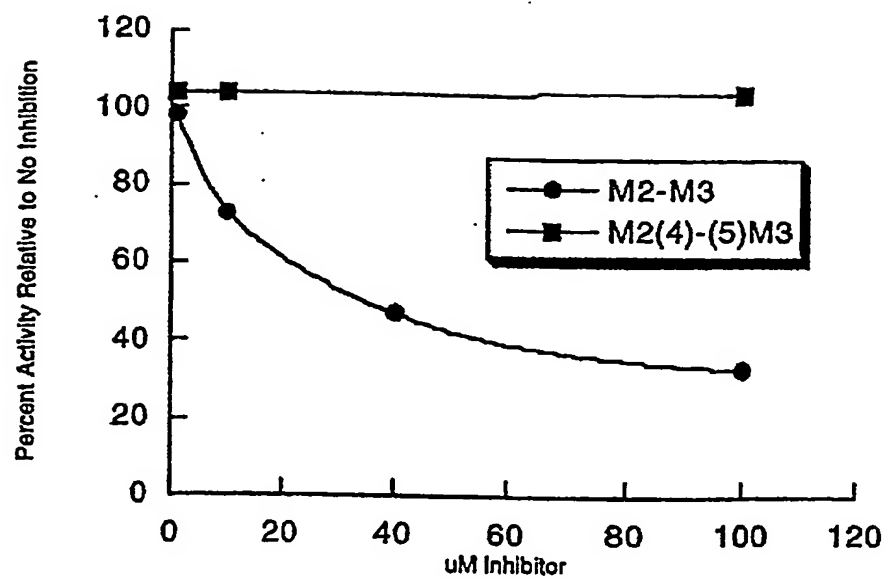


Figure 8



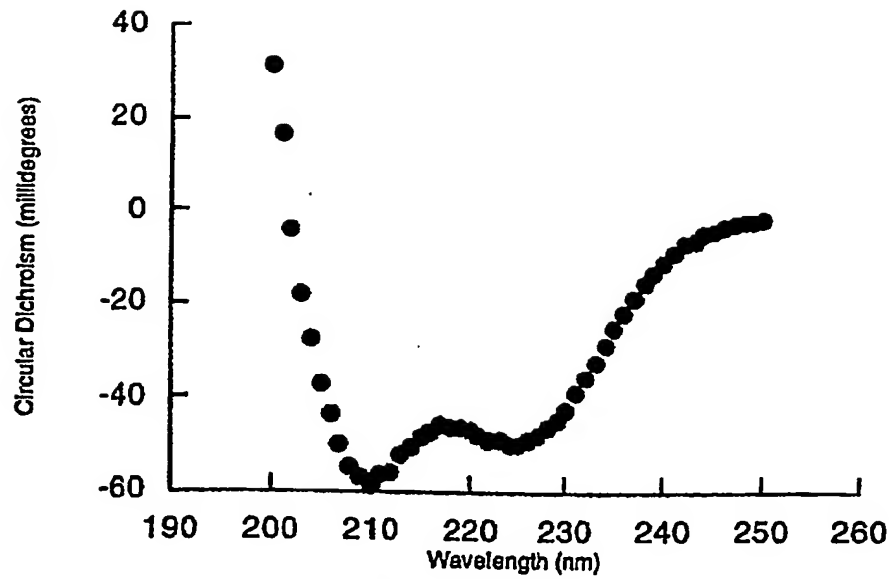
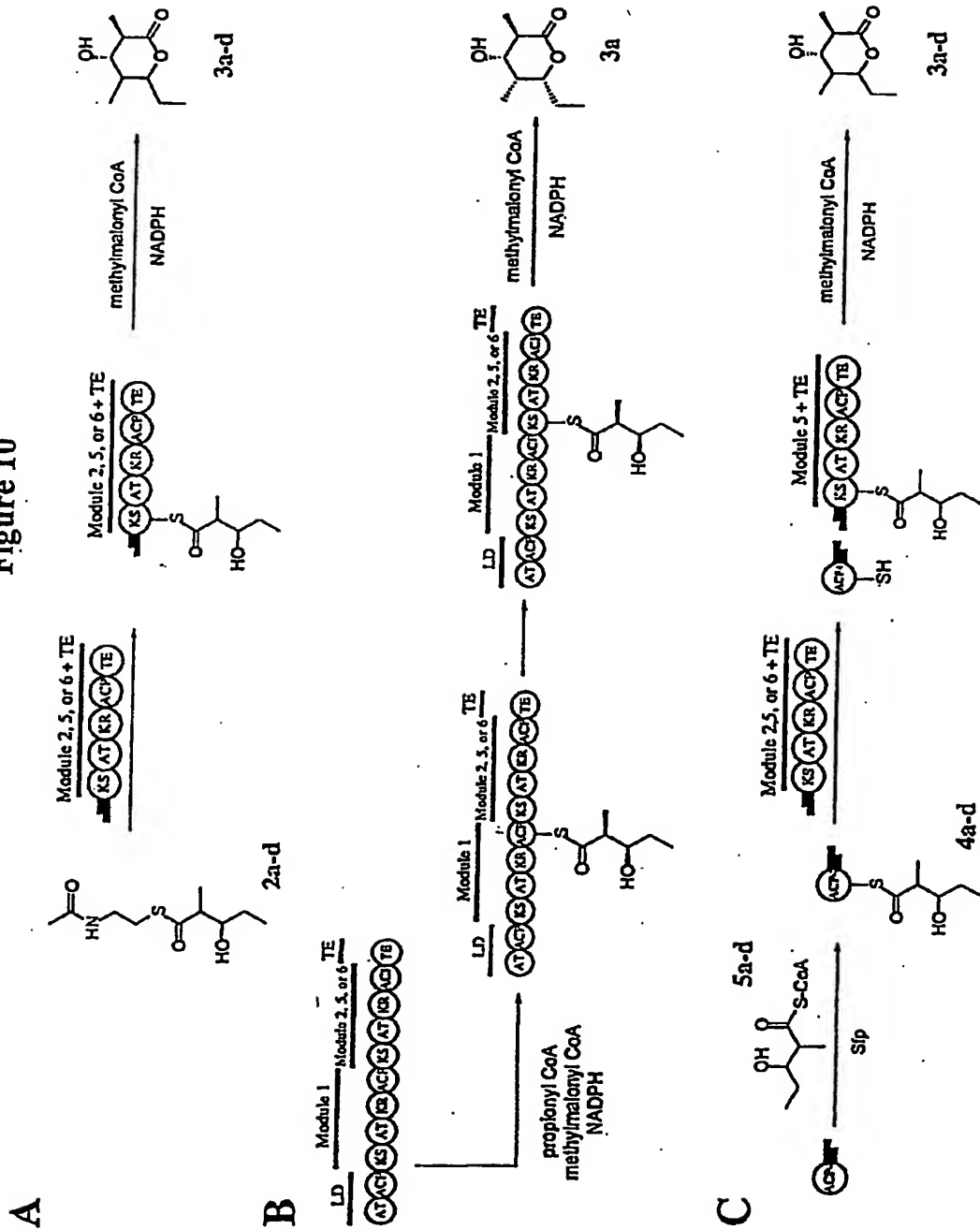


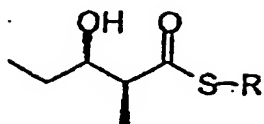
Figure 9

Figure 10

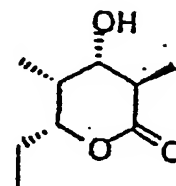


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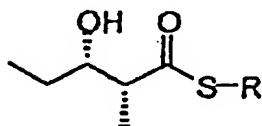
PCT/US03/06910



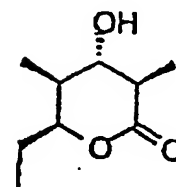
2a: R=N-acetylcysteamine  
4a: R=Acyl carrier protein



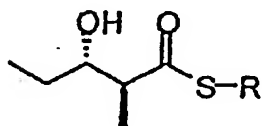
3a



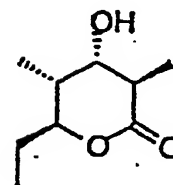
2b: R=N-acetylcysteamine  
4b: R=Acyl carrier protein



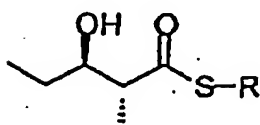
3b



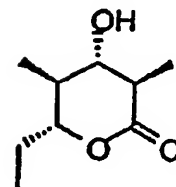
2c: R=N-acetylcysteamine  
4c: R=Acyl carrier protein



3c



2d: R=N-acetylcysteamine  
4d: R=Acyl carrier protein



3d

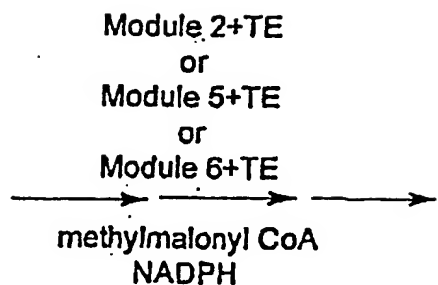


Figure 11

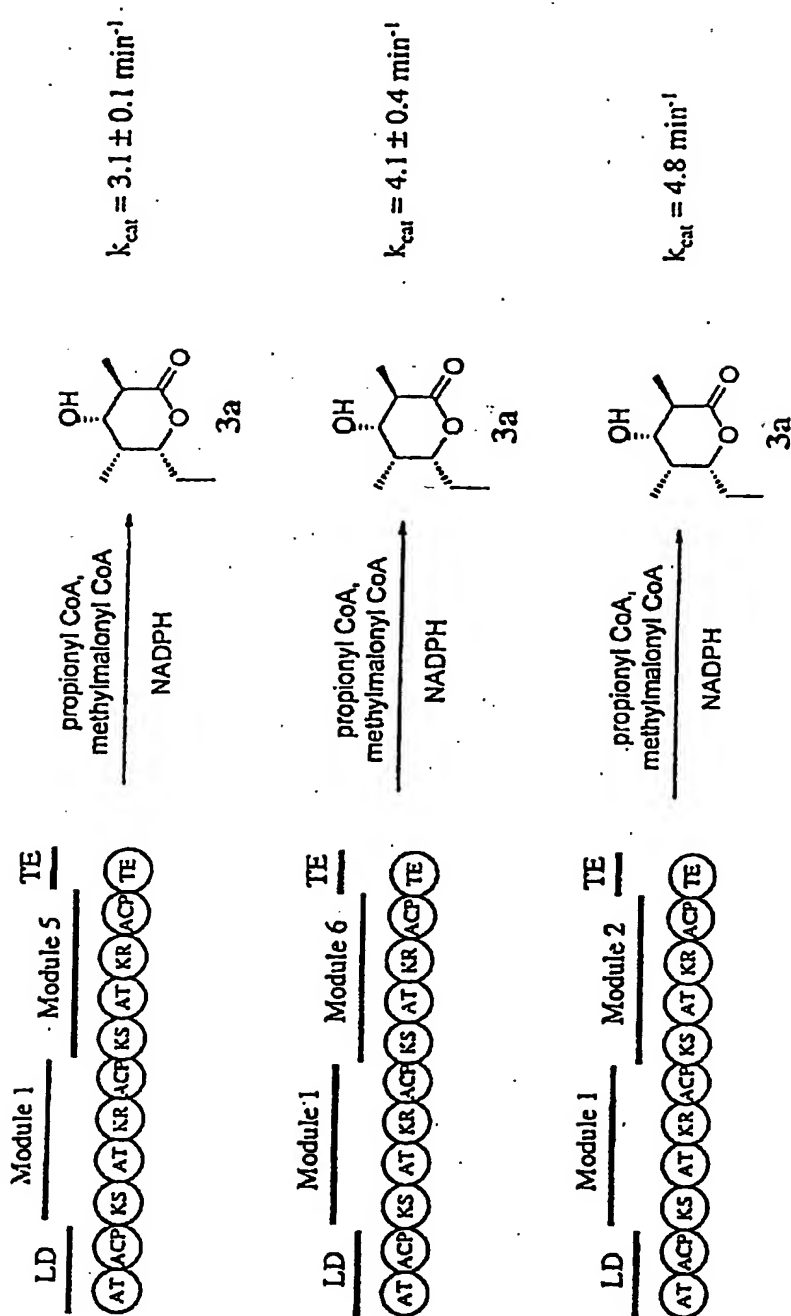


Figure 12




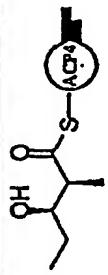
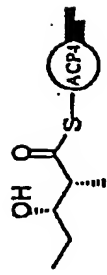
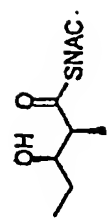
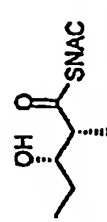
Substrate	(5)Module 2 + TE 	(5)Module 5 + TE 	(5)Module 6 + TE 
4a 	2900 ± 500	290 ± 50	340 ± 60
4b 	18 ± 1	3.9 ± 0.7	85 ± 15
2a 	0.75 ± 0.01	0.016 ± 0.002	1.1 ± 0.1
2b 	0.0076 ± 0.0006	0.0011 ± 0.0001	0.058 ± 0.006

Figure 13

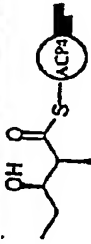
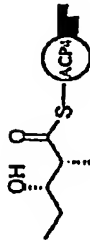
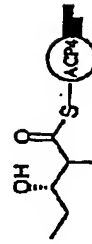
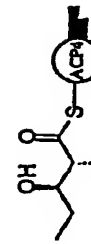
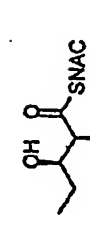
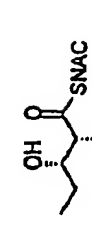
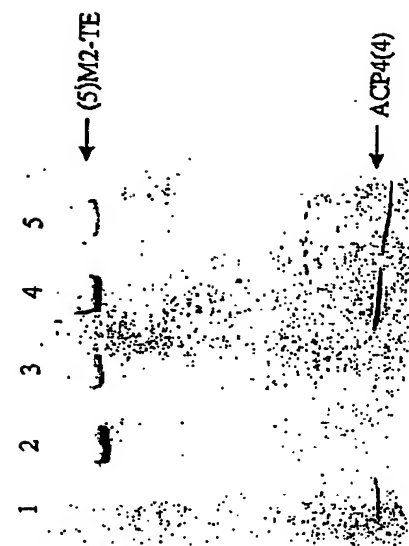
Substrate	(5)Module 2 + TE		(5)Module 5 + TE		(5)Module 6 + TE	
						
4a	$6.7 \pm 0.2$	$> 9.3 \pm 1.4$	$> 10 \pm 1$			
4b	$> 0.97 \pm 0.02$	$> 0.48 \pm 0.02$	$> 3.4 \pm 0.4$			
4c	$> 1.0 \pm 0.1$	$> 1.4 \pm 0.1$	$> 2.1 \pm 0.2$			
4d	$> 0.29 \pm 0.03$	$> 0.20 \pm 0.01$	$> 1.9 \pm 0.1$			
2a	$> 4.6 \pm 0.6$	$0.24 \pm 0.01$	$17 \pm 2.9$			
2b	$0.25 \pm 0.02$	$0.017 \pm 0.001$	$2.4 \pm 0.2$			
2c	N.D.	N.D.	N.D.			
2d	N.D.	N.D.	N.D.			

Figure 14



Lane	ACP	Module	<sup>14</sup> C-Label	Extender Unit
1	holo-ACP4(4)	none	* 2 a	none
2	none	(5)M2+TE	* 2 a	none
3	none	(5)M2+TE	* 2 a	methylmalonyl-CoA
4	holo-ACP4(4)	(5)M2+TE	* 2 a	none
5	holo-ACP4(4)	(5)M2+TE	* 2 a	methylmalonyl-CoA

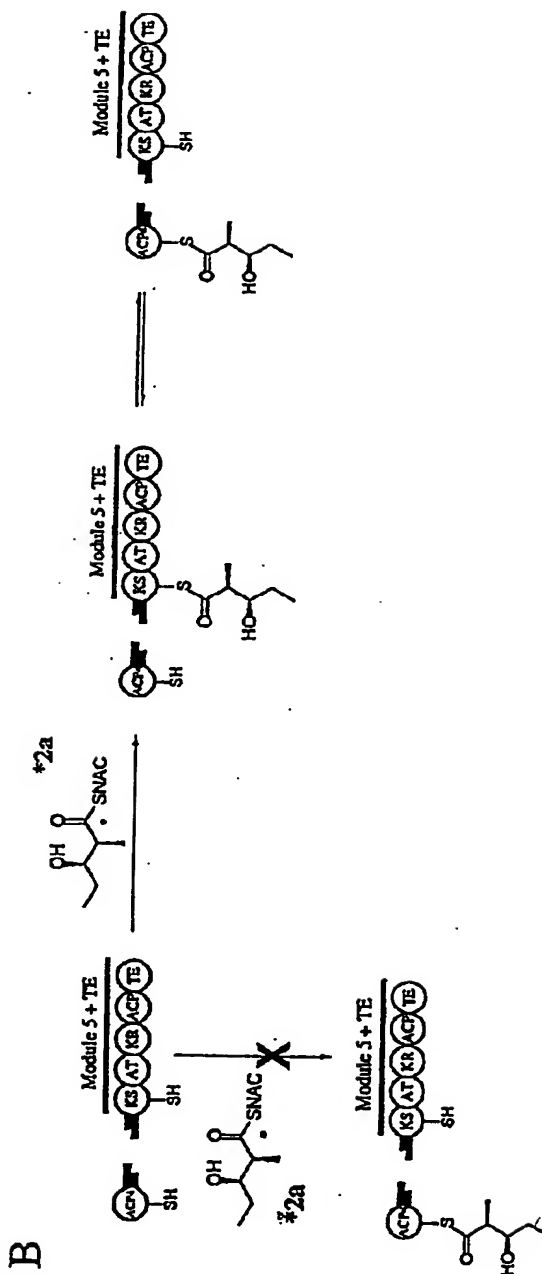


Figure 15

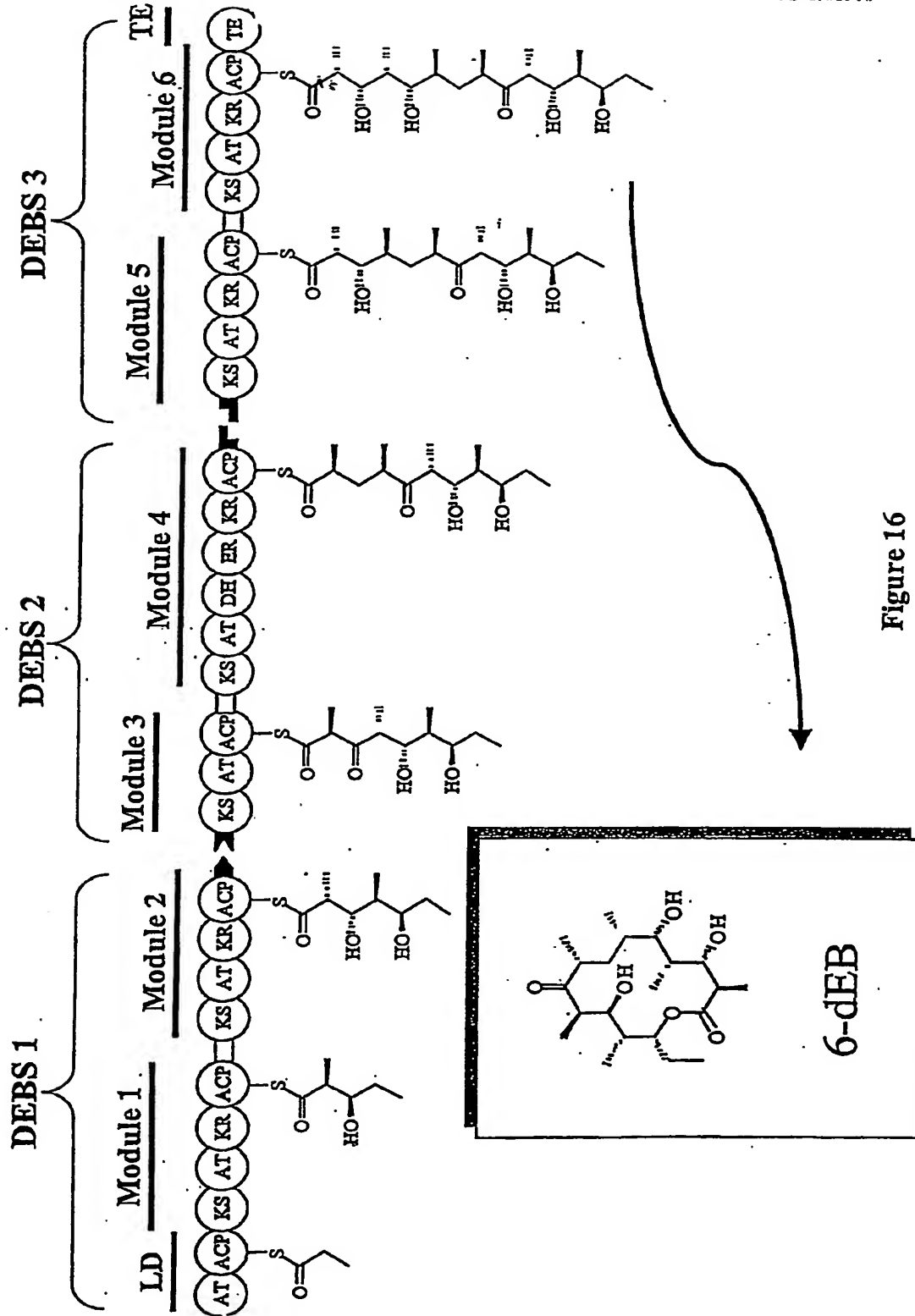


Figure 16



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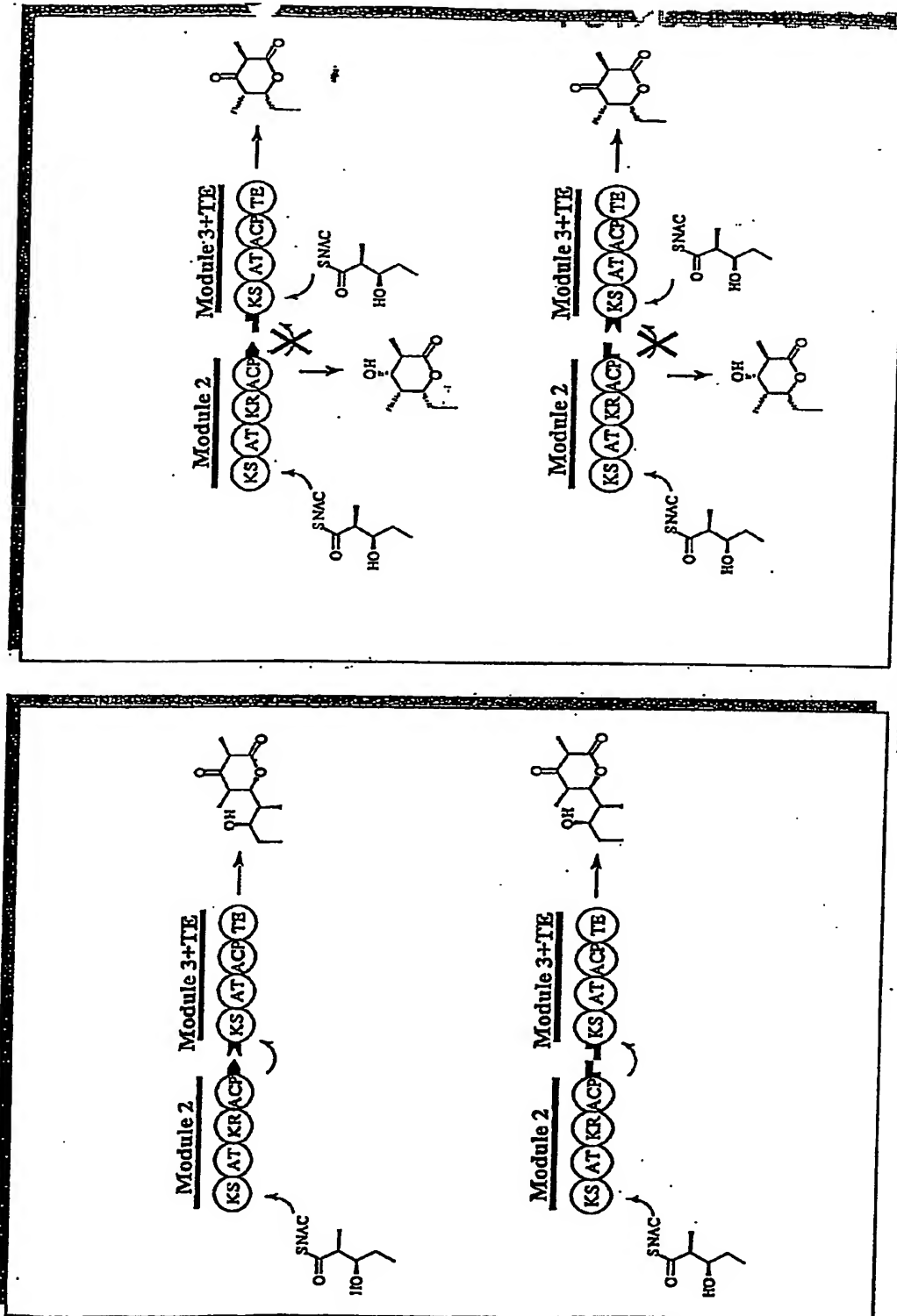


Figure 17

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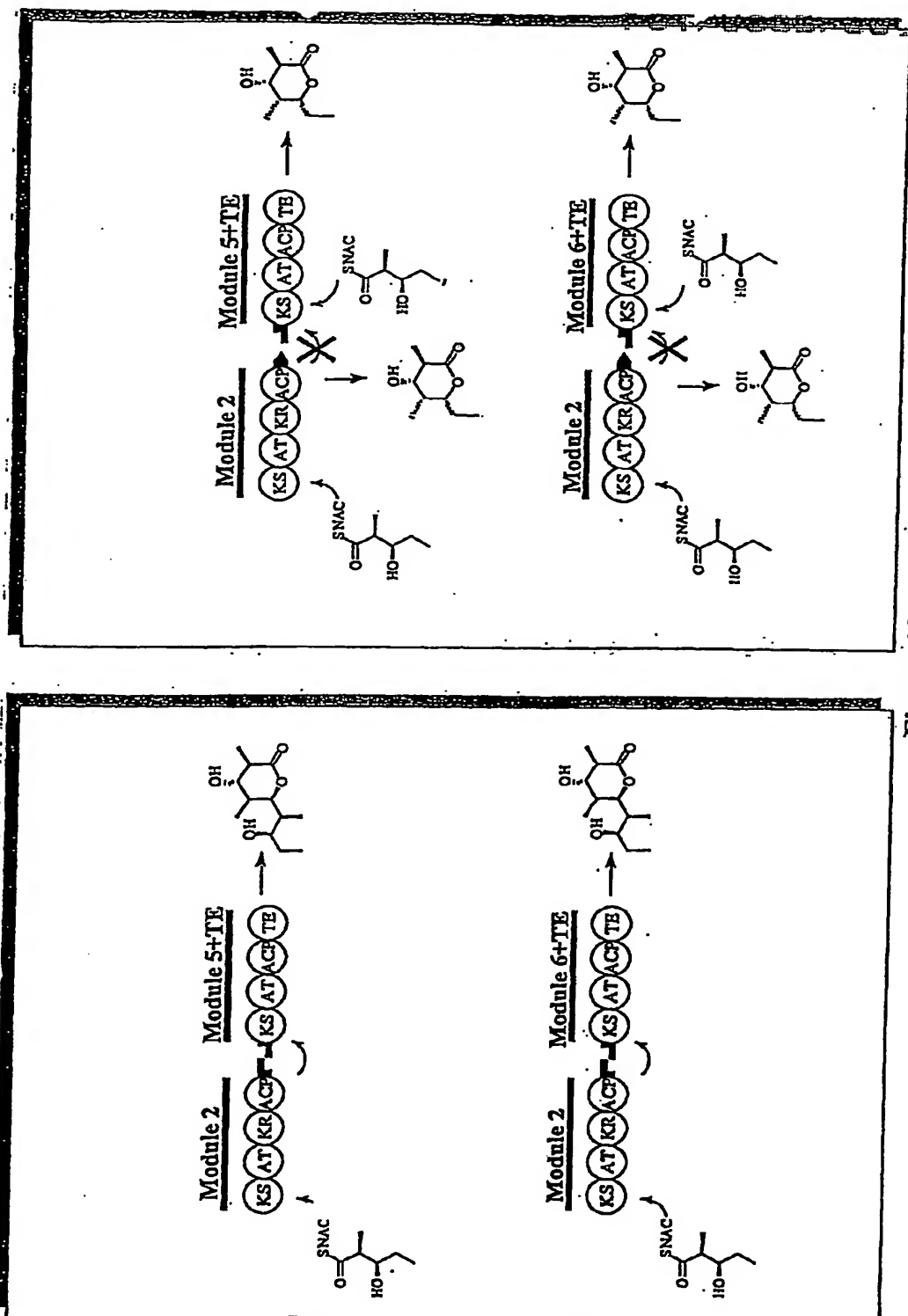


Figure 18

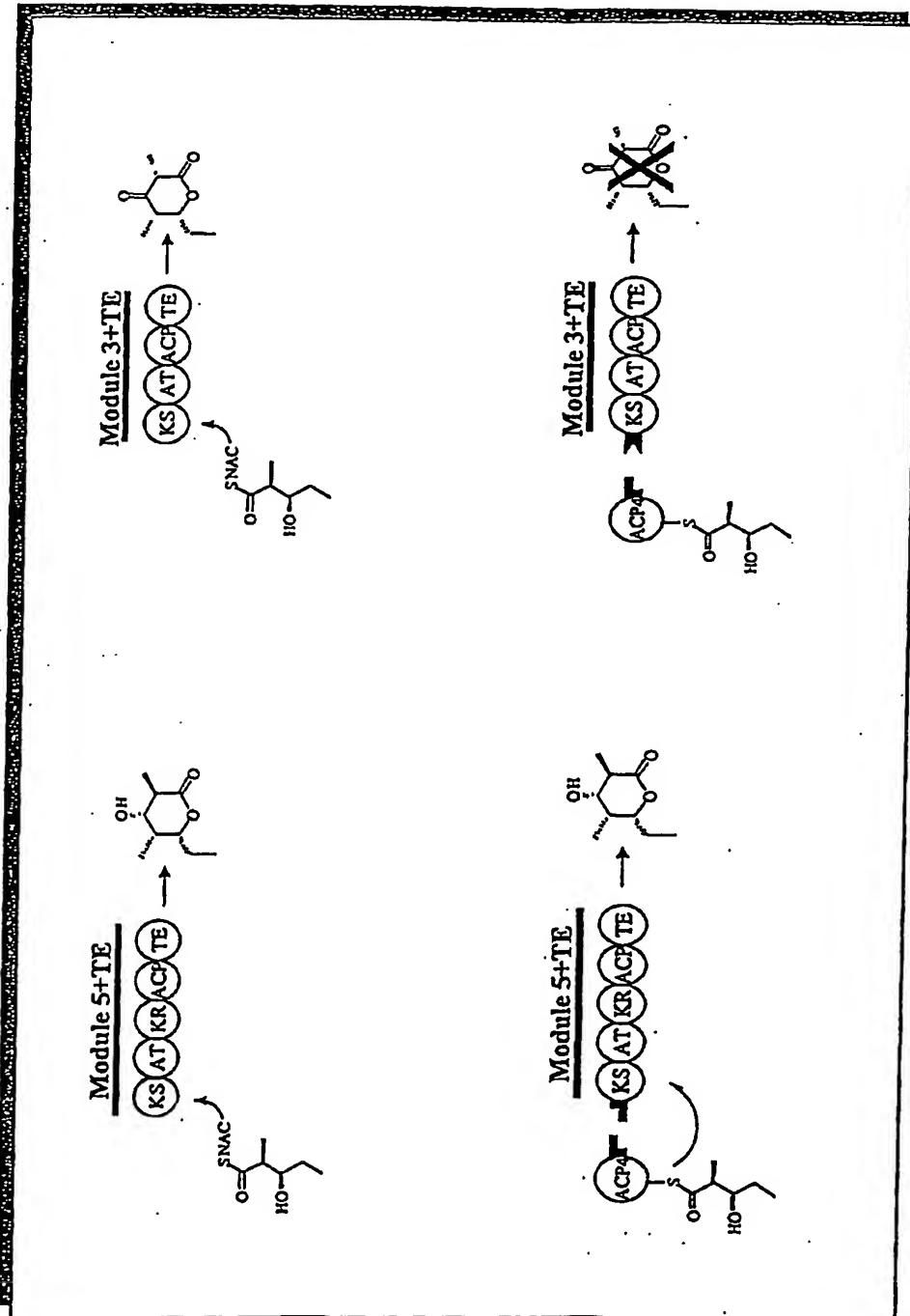
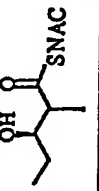
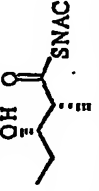
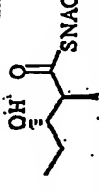
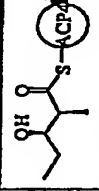
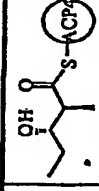
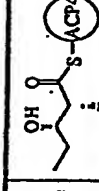
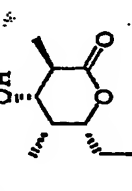
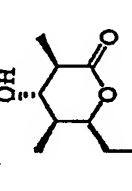
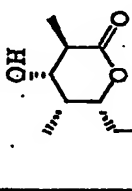
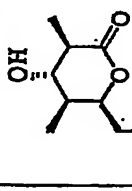
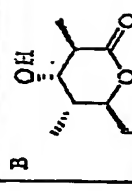
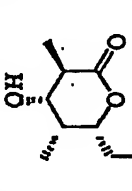
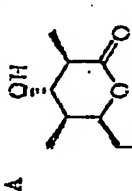
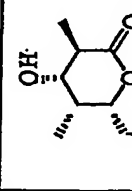
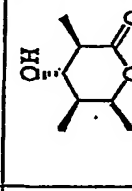
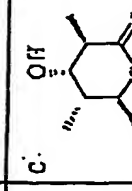


Figure 19

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Figure 20

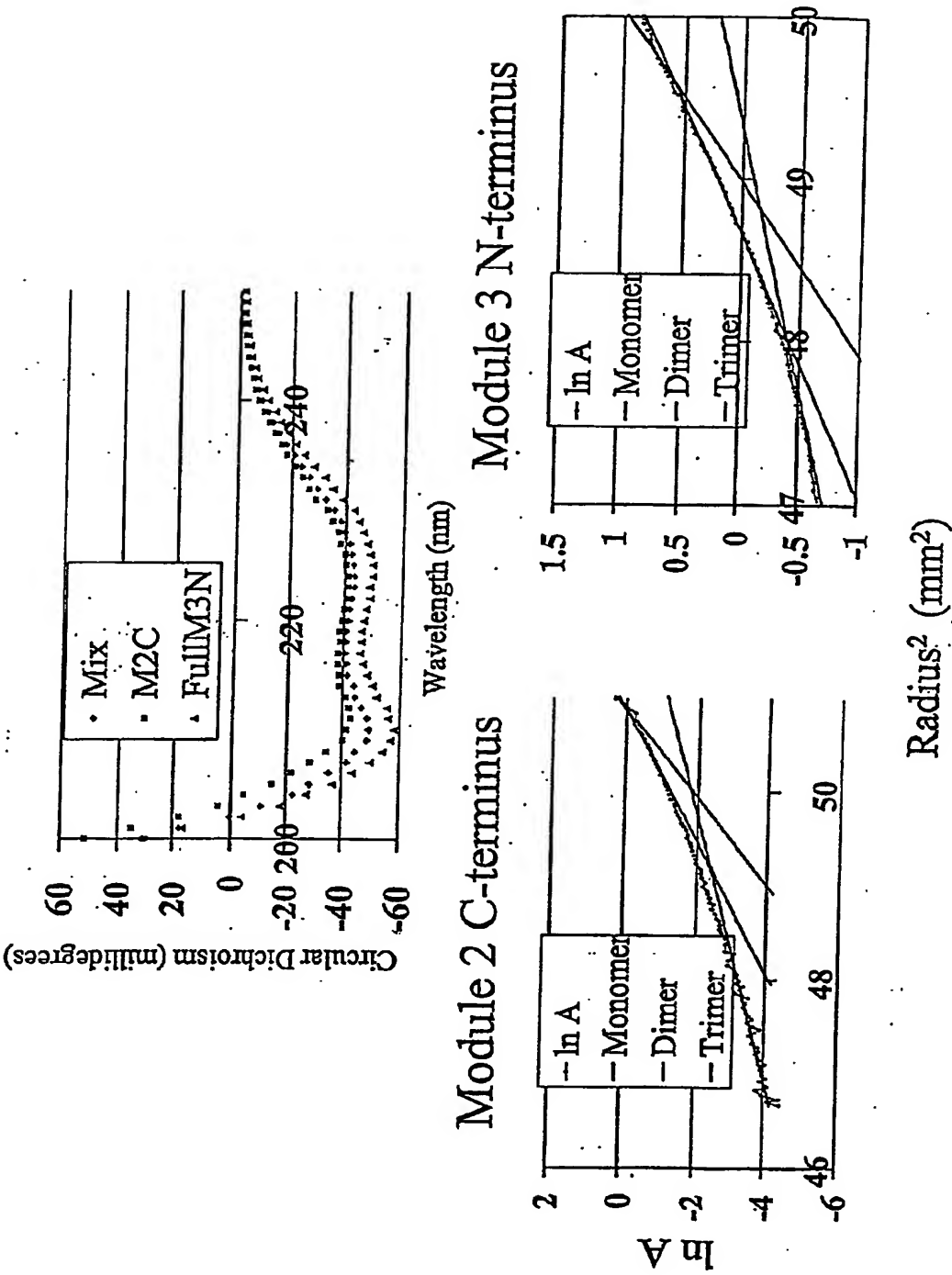
Substrates Enzyme						
Module 2 + TE KS AT KR AC TE			X			
Module 5 + TE KS AT KR AC TE			X			

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Figure 21

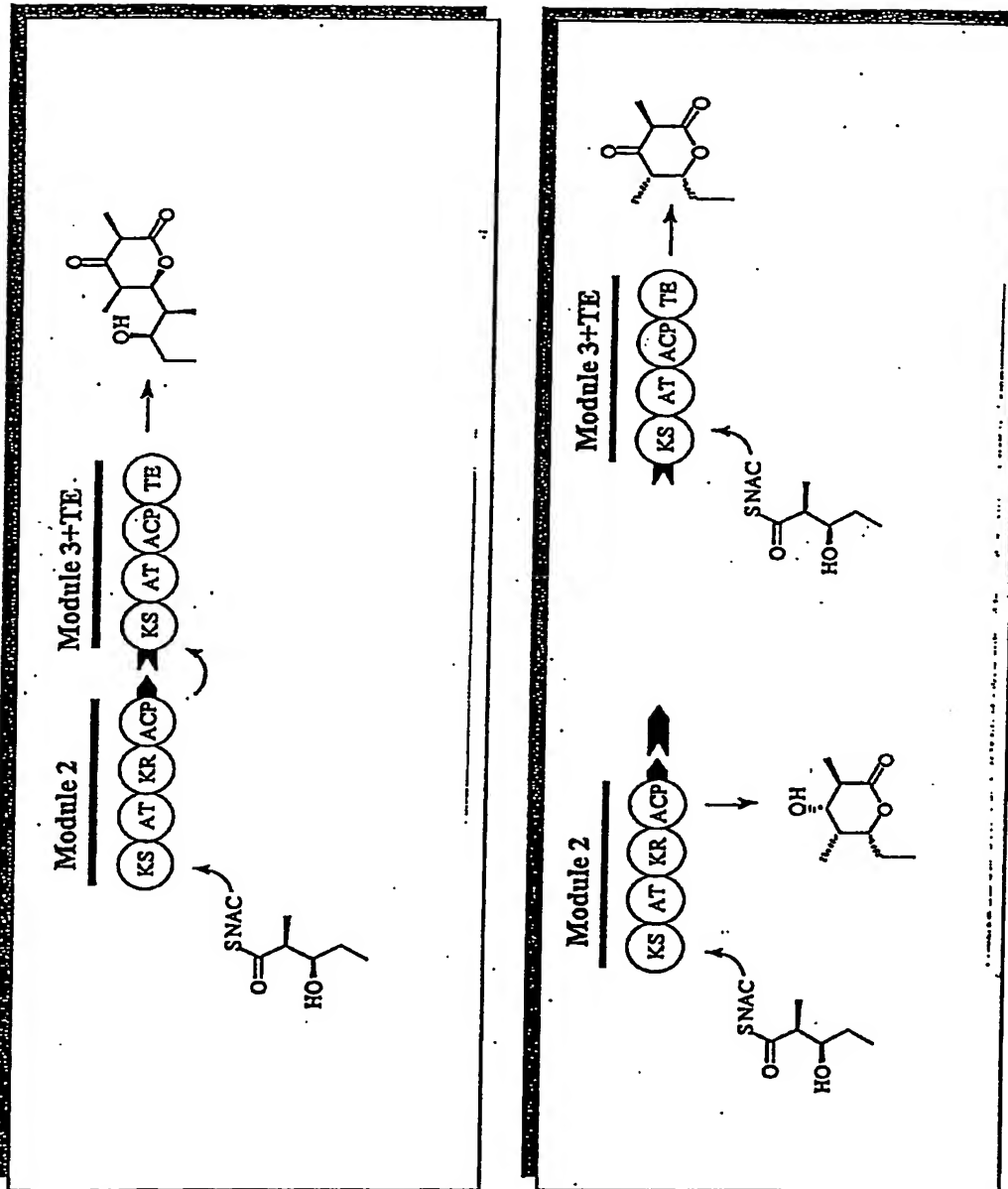


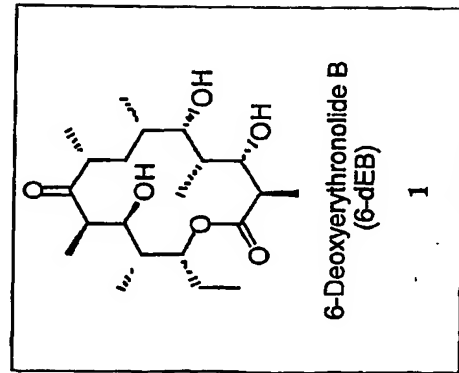
10/506630

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Figure 22





### Figure 23

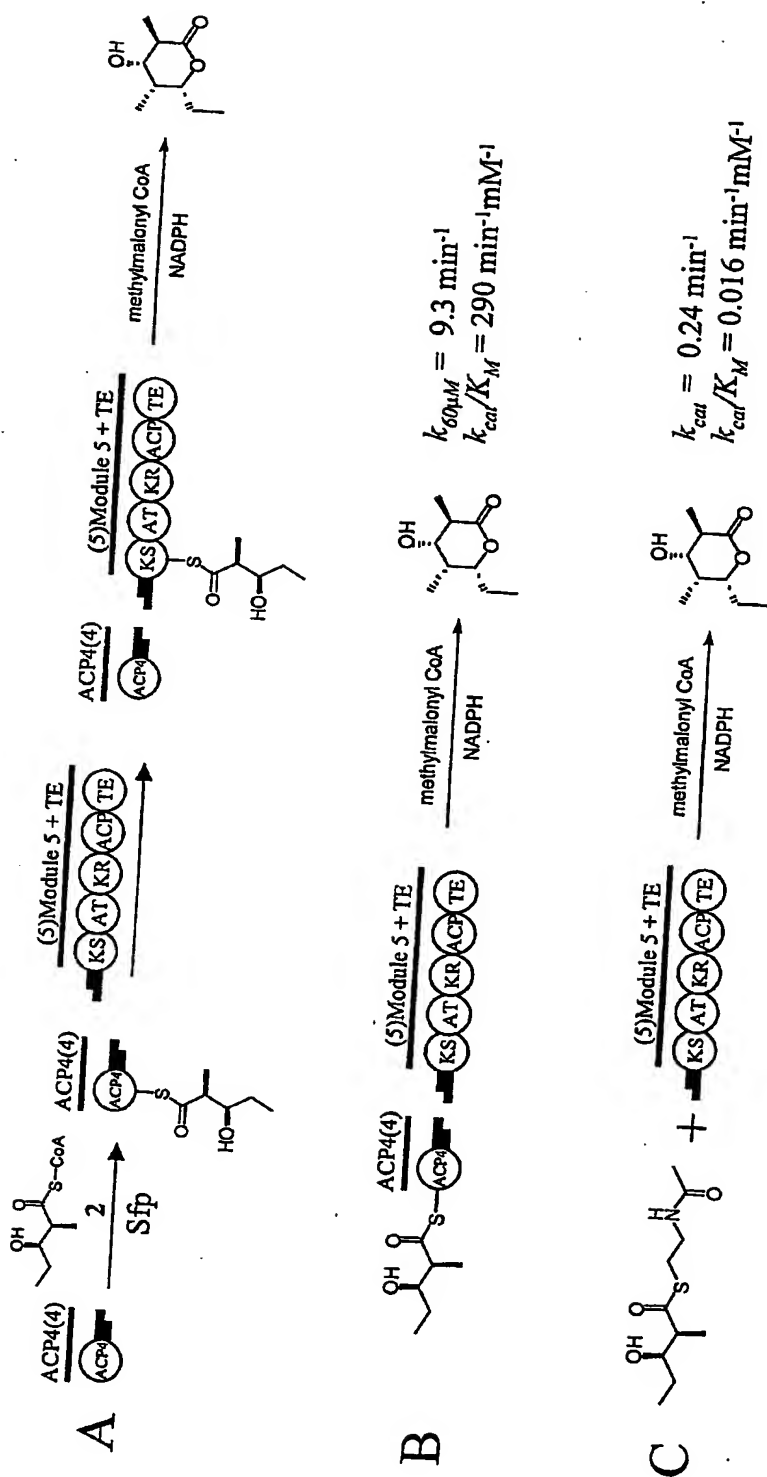


Figure 24



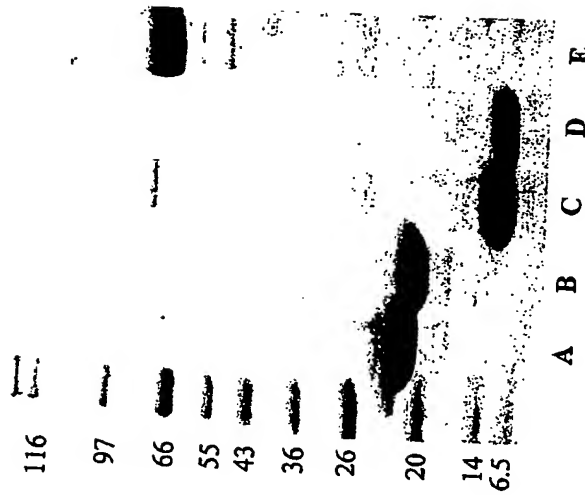


Figure 25

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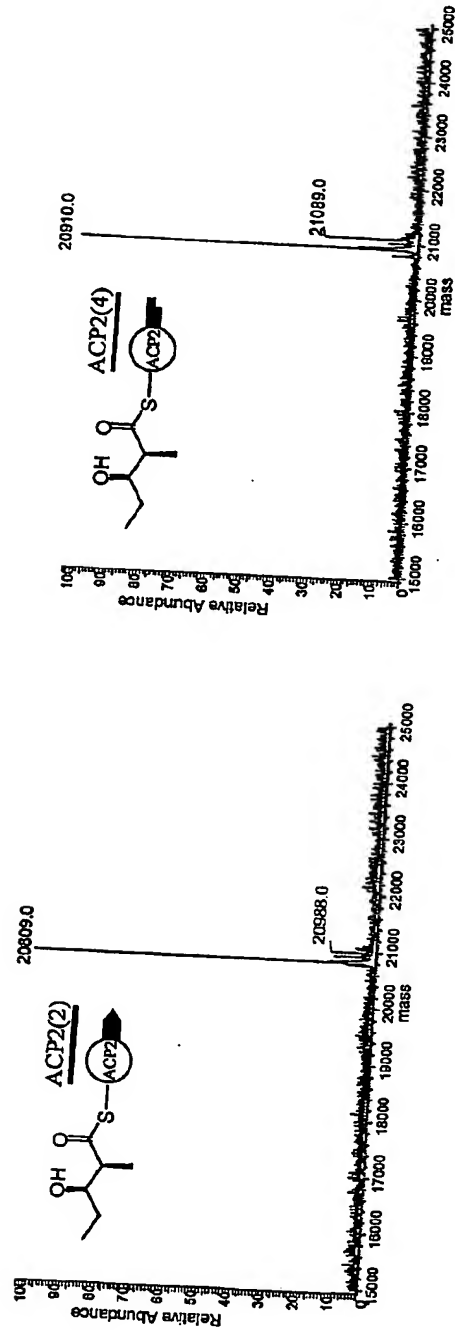
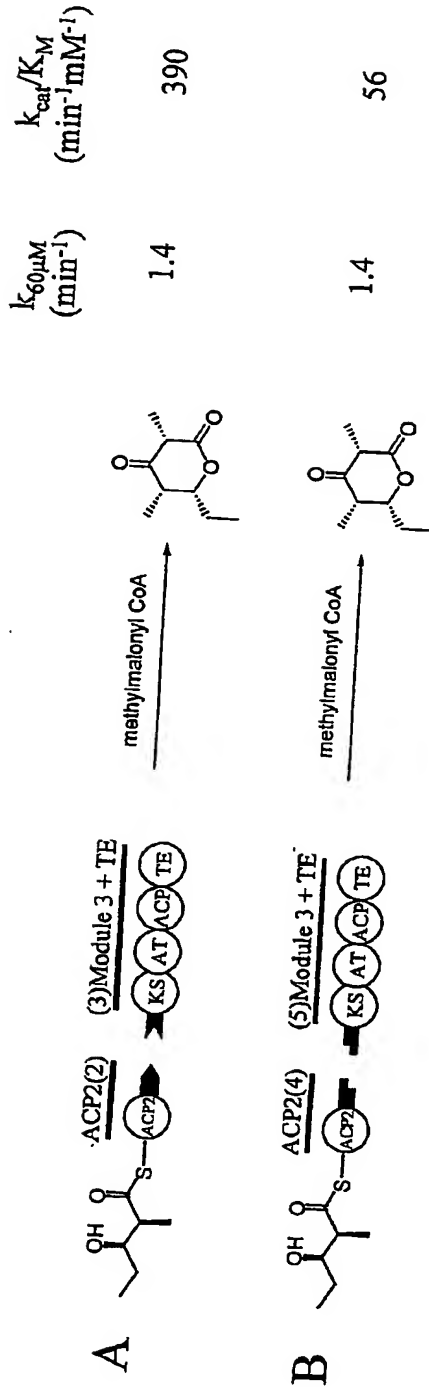


Figure 26

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$k_{cat}/K_M$ ( $\text{min}^{-1}\text{mM}^{-1}$ )	$k_{50\mu\text{M}}$ ( $\text{min}^{-1}$ )	
390	1.4	
6.5	0.52	
2.0	0.33	
N.D.	N.D.	

Figure 27

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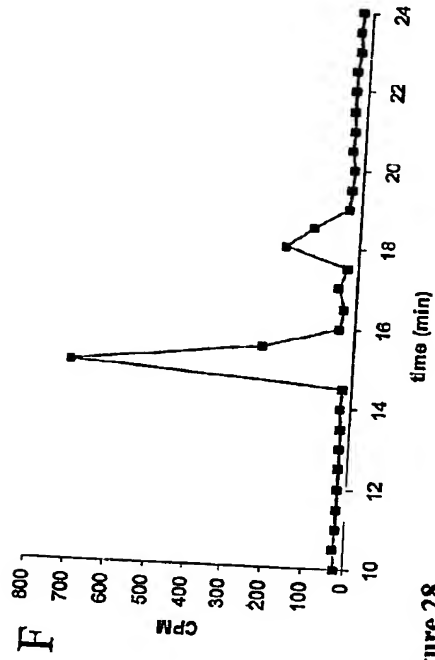
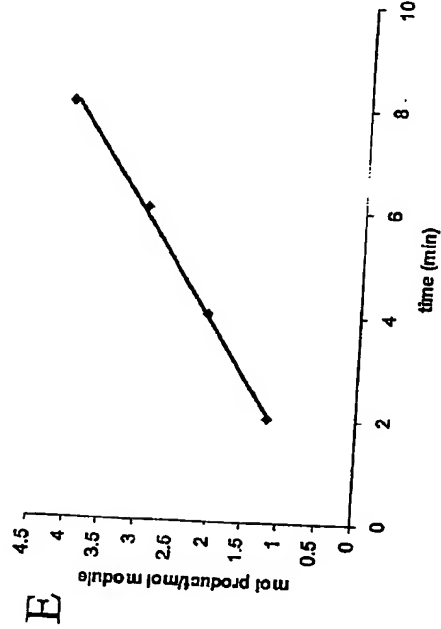
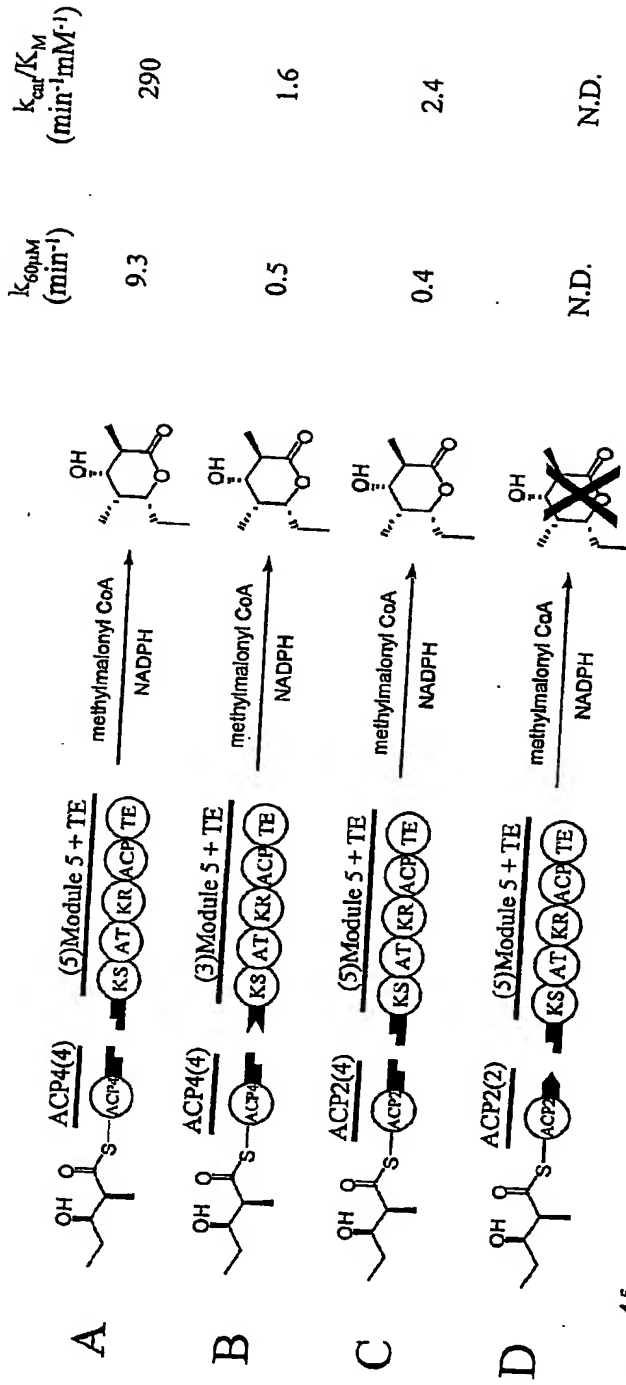


Figure 28

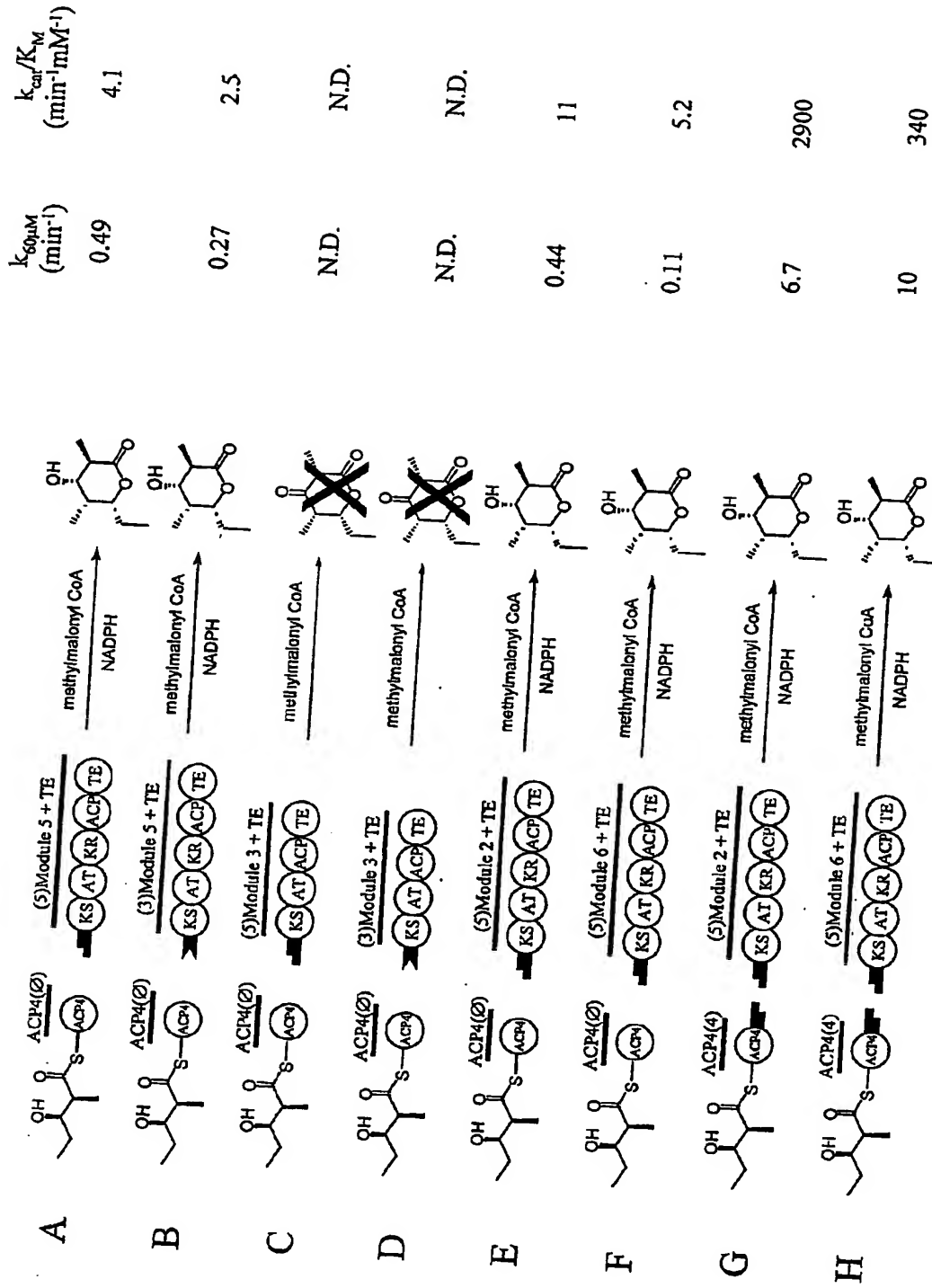
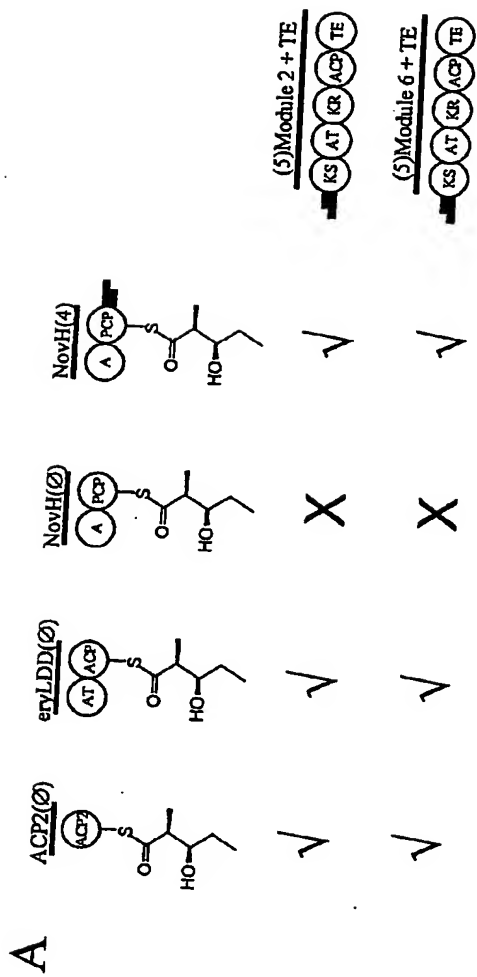


Figure 29

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**B**

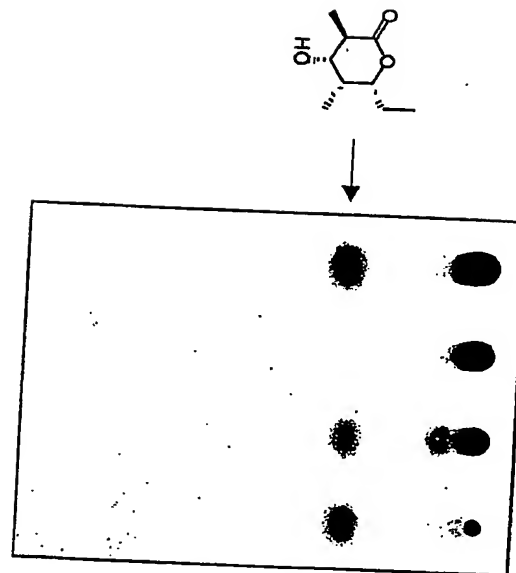


Figure 30

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1	AAPOH VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	- 600			
2	APVUS	I-I	GMA-L	EV DS	TSGRDSAAEV	-D	VPDE	IMASD...	AGTRAH-KEM	AG-GD	AR	-2071			
3	ELES	I-I	SHA-L	GV NT	REGGETLGGP	-D	DLAR	LEHEDPDRSG	TSYVOK-GEN	DD-AG	AE	- 126			
4	ADSES	I-I	GIG-F	GI GS	AEGANITGP	-A	DIGR	LYHEDPDRSG	TSYVOK-GEN	TD-AD	PC	-1584			
5	BRAGE	I-I	GMA-F	DV DS	SGGDAIAEA	-A	EPD	.....	PDARL-GH	AA-GD	AG	- 122			
6	KRADD	I-I	GMA-F	GV HE	VGRDAVTEH	-A	DLOA	LFOPDRSG	TSYSRE-AE	DG-AL	AE	-1581			
1	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 700			
2	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-2171			
3	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 225			
4	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-1684			
5	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 222			
6	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-1680			
1	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 800			
2	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-2271			
3	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 325			
4	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-1784			
5	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 322			
6	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-1780			
1	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 898			
2	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-2371			
3	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 425			
4	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-1882			
5	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	- 422			
6	ISVIL	SG	EVTE	BRQG	SA	SA	SA	SA	SA	SA	SA	-1880			
1	EPN	BAAGAP	RRR	SSB	STW	FALE	EAPQV...	EGERVEAGD	VVAE	VLSB	SAEGRACIA	RIAAHLEEF	GODPROIAYS	ETGRAALPH	- 992
2	RE	BAAGAP	RRR	SSB	STW	FALE	EAPQV...	EGERVEAGD	VVAE	VLSB	SAEGRACIA	RIAAHLEEF	GODPROIAYS	ETGRAALPH	-2469
3	CP	BAAGAP	RRR	SSB	STW	FALE	EAPQV...	EGERVEAGD	VVAE	VLSB	SAEGRACIA	RIAAHLEEF	GODPROIAYS	ETGRAALPH	- 518
4	VP	BAAGAP	RRR	SSB	STW	FALE	EAPQV...	EGERVEAGD	VVAE	VLSB	SAEGRACIA	RIAAHLEEF	GODPROIAYS	ETGRAALPH	-1974
5	RS	BAAGAP	RRR	SSB	STW	FALE	EAPQV...	EGERVEAGD	VVAE	VLSB	SAEGRACIA	RIAAHLEEF	GODPROIAYS	ETGRAALPH	- 515
6	SP	BAAGAP	RRR	SSB	STW	FALE	EAPQV...	EGERVEAGD	VVAE	VLSB	SAEGRACIA	RIAAHLEEF	GODPROIAYS	ETGRAALPH	-1978
1	AAPOH	VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	- 106		
2	AAPOH	VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	-1089		
3	AAPOH	VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	-2559		
4	AAPOH	VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	- 612		
5	AAPOH	VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	-2066		
6	AAPOH	VAVV	AMACRLGGV	STDE	SEGRDAVAGL	PTGMDLOS	LHEDPDRSG	TABRGOGCH	TEANA	TPH	PNSEHRLA	MOHCLNTE	- 603		
1	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 204			
2	APSL	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-1184			
3	APSL	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2659			
4	APSL	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 710			
5	APSL	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2164			
6	APSL	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 701			
1	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2166			
2	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 303			
3	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-1284			
4	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2758			
5	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 809			
6	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2263			
1	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 800			
2	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2265			
3	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 398			
4	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-1381			
5	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	-2853			
6	ALSTE	D-V	VL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	EL-SUM	- 906			
1	LEP	VARRS	TE	.....	RI	EMPTGA	.....	GEP	ARLDGTILVA	KYAGTADETS	TAA.RE	-1439			
2	LEP	VARRS	TE	.....	RI	EMPTGA	.....	GEP	ARLDGTILVA	KYAGTADETS	TAA.RE	-2908			
3	LEP	VARRS	TE	.....	RI	EMPTGA	.....	GEP	ARLDGTILVA	KYAGTADETS	TAA.RE	- 957			
4	LEP	VARRS	TE	.....	RI	EMPTGA	.....	GEP	ARLDGTILVA	KYAGTADETS	TAA.RE	-2392			
5	LEP	VARRS	TE	.....	RI	EMPTGA	.....	GEP	ARLDGTILVA	KYAGTADETS	TAA.RE	- 952			
6	LEP	VARRS	TE	.....	RI	EMPTGA	.....	GEP	ARLDGTILVA	KYAGTADETS	TAA.RE	-2399			

Figure 31 A

**PCT/US03/06910**

**Figure 31 B**



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